

Amendments to the Claims:

This listing of claims will replace all prior versions, and listings, of claims in the application:

Listing of Claims:

1. (original) A method for identifying a polynucleotide sequence, wherein the polynucleotide sequence may be associated with a commercially or aesthetically relevant trait, comprising:
 - a) aligning homologous nucleotide sequences of at least two individual organisms, wherein said at least two individual organisms are selected from the group consisting of individual organisms of a single strain, individual organisms of different strains, individual organisms of the same species, individual organisms of different species, and any combination of the foregoing, wherein one nucleotide sequence is associated with an individual organism exhibiting said commercially or aesthetically relevant trait; and
 - b) detecting a region of polynucleotide sequence for which the number of nucleotide differences/site indicates an evolutionary bottleneck; whereby a polynucleotide sequence associated with a commercially or aesthetically relevant trait of said organism may be identified.
2. (cancelled)
3. (original) A method for identifying a polynucleotide sequence encoding a polypeptide, wherein the polypeptide may be associated with a commercially or aesthetically relevant trait comprising:
 - a) aligning homologous protein-coding nucleotide sequences of at least two individual organisms, wherein said at least two individual organisms are selected from the group consisting of individual organisms of a single strain, individual organisms of different strains, individual organisms of the same species, individual organisms of different species, and any combination of the foregoing, wherein one nucleotide sequence encodes a polypeptide associated with an domesticated organism exhibiting said commercially or aesthetically relevant trait; and
 - b) detecting a region of polynucleotide sequence for which the number of nucleotide differences/site indicates an evolutionary bottleneck; whereby a polynucleotide sequence associated with a commercially or aesthetically relevant trait of said organism may be identified.

4. (cancelled)

5. (currently amended) ~~A-The method of claim 1, further comprising for identifying a regulatory element comprising:~~
~~comprising:~~

- a) ~~aligning homologous nucleotide sequences of at least about two at least two individual organisms, wherein said at least two individual organisms are selected from the group consisting of individual organisms of a single strain, individual organisms of different strains, individual organisms of the same species, individual organisms of different species, and any combination of the foregoing; and~~
- ~~b) detecting a region of polynucleotide sequence for which the number of nucleotide differences/site indicates an evolutionary bottleneck;~~
- c) determining that the region identified in b) is a non-coding region, wherein the polynucleotide sequence is a whereby a regulatory element is identified.

6. (currently amended) The method according to ~~any one of claims 1-4~~claim 1, wherein the identifying the number of nucleotide differences/site is calculated by $\pi = 1/[n(n-1)/2] \sum_{i < j} \Pi_{ij} / L$, n is number of sequences, where i and j represent any two sequences being compared in a series of sequences and L = sequence length.

7. (currently amended) The method according to ~~any one of claims 1-4~~claim 1, further comprising determining if the region displays a signature of positive selection.

8. (currently amended) The method of Claim 9~~7~~, wherein said determining comprises calculating a Ka/Ks value.

10.9. (currently amended) The method according to ~~any one of claims 1-4~~claim 1, wherein the method is performed in an automated pipeline.

11.10. (currently amended) The method according to ~~any one of claims 1-4~~ claim 1, wherein the at least two strains and/or individuals of a single strain is at least ten strains and/or individuals of a single strain.

12.11. (currently amended) The method of Claim 11.10, wherein the at least two strains and/or individuals of a single strain is at least fifteen strains and/or individuals of a single strain.

13.12. (currently amended) A method for identifying an agent which may modulate a commercially or aesthetically relevant trait that is unique, enhanced or altered in the domesticated organism as compared to other domesticated or ancestral species of the domesticated organism, said method comprising contacting at least one candidate agent with a cell, model system or transgenic plant or animal that expresses a polynucleotide sequence that is an evolutionary bottleneck, wherein the agent is identified by its ability to modulate function of the polypeptide encoded by the polynucleotide.

14.13. (currently amended) A method for correlating a nucleotide sequence which is an evolutionary bottleneck to a commercially or aesthetically relevant trait that is unique, enhanced or altered in a domesticated organism, comprising:

- a) identifying a nucleotide sequence which is an evolutionary bottleneck; and
- b) analyzing the functional effect of the presence or absence of the identified sequence in the domesticated organism or in a model system.

14. (new) The method of claim 1, wherein the polynucleotide sequence is a regulatory element.

15. (new) The method according to claim 3, wherein the identifying the number of nucleotide differences/site is calculated by $\pi = 1/[n(n-1)/2] \sum_{i < j} \Pi_{ij} / L$, n is number of sequences, where i and j represent any two sequences being compared in a series of sequences and L = sequence length.

16. (new) The method according to claim 3, further comprising determining if the region displays a signature of positive selection.

17. (new) The method of Claim 16, wherein said determining comprises calculating a Ka/Ks value.

18. (new) The method according to claim 3, wherein the method is performed in an automated pipeline.

19. (new) The method according to claim 3, wherein the at least two strains and/or individuals of a single strain is at least ten strains and/or individuals of a single strain.

20. (new) The method of claim 3, wherein the at least two strains and/or individuals of a single strain is at least fifteen strains and/or individuals of a single strain.